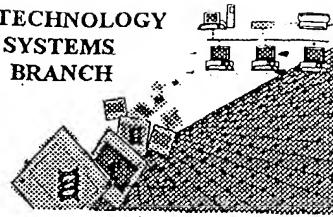


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



RAW SEQUENCE LISTING  
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101674,124  
Source: CD  
Date Processed by STIC: 10-8-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk~~CD~~-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <i>10/674,134</i>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed 72 characters</b> in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use <b>space characters</b> , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only <b>valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) <i>27087 27410</i> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



II

RAW SEQUENCE LISTING DATE: 10/08/2003  
PATENT APPLICATION: US/10/674,124 TIME: 13:16:54

Input Set : D:\seqlist.txt  
Output Set: N:\CRF4\10082003\J674124.raw

3 <110> APPLICANT: INOKO, Hidetoshi  
 4 TAMIYA, Gen  
 7 <120> TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE  
 8 GENETIC POLYMORPHISM MARKERS  
 11 <130> FILE REFERENCE: TECH-003CIP  
 > 13 <140> CURRENT APPLICATION NUMBER: US/10/674,124  
 14 <141> CURRENT FILING DATE: 2003-09-26  
 16 <150> PRIOR APPLICATION NUMBER: 10/257,511  
 17 <151> PRIOR FILING DATE: 2003-03-07  
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP00/07621  
 20 <151> PRIOR FILING DATE: 2000-10-30  
 22 <150> PRIOR APPLICATION NUMBER: JP2000-112699  
 23 <151> PRIOR FILING DATE: 2000-04-13  
 25 <150> PRIOR APPLICATION NUMBER: JP2002-327516  
 26 <151> PRIOR FILING DATE: 2002-09-28  
 28 <150> PRIOR APPLICATION NUMBER: JP2002-383869  
 29 <151> PRIOR FILING DATE: 2002-12-09  
 31 <160> NUMBER OF SEQ ID NOS: 27110  
 33 <210> SEQ ID NO: 1  
 34 <211> LENGTH: 466  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Homo sapiens  
 38 <220> FEATURE:  
 39 <223> OTHER INFORMATION: chr8.fa.07frz.212765  
 41 <220> FEATURE:  
 42 <223> OTHER INFORMATION: Located on chromosome 1  
 44 <220> FEATURE:  
 45 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 46 chromosomal short arm and 5'-terminus of this base  
 47 sequence : 8211  
 49 <220> FEATURE:  
 50 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 51 sequence listing upward to telomere on chrosomal short arm and  
 52 5'-terminus of this base sequence : 0  
 54 <400> SEQUENCE: 1  
 55 agatggatga tagatcattg atagatgata ggttagatgt agatagatta tagtagata 60  
 57 aatagatgga ttagatggatgg atgatagata cttgattgtat agatgatagg tagatagtag 120  
 59 atagatgata gataatgata gatgatagct agatagtaga tagatgtgtat agtagatgg 180  
 61 tagatagaga ttagatgataga tggatgatag atggatggat ggtatgatagg tgattgtatag 240  
 63 atggatgata ggtggatggat agagatggta gataaataga tggatgatgg atggatgata 300  
 65 gagagctgat agtagataag gtagatgatgat gatagatgtat agatggatgg atgatagatg 360  
 67 attgatagag agatagagag agaaggatga tagactgagc atcataactt cactgaatgc 420  
 69 taccatgttgg attcaaaaatgt caqcaaaactq aaacqtcqaa tttcaq 466

P.6

Does Not Comply  
Corrected Diskette Needed

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/674,124

DATE: 10/08/2003

TIME: 13:16:54

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

72 <210> SEQ ID NO: 2  
 73 <211> LENGTH: 207  
 74 <212> TYPE: DNA  
 75 <213> ORGANISM: Homo sapiens  
 77 <220> FEATURE:  
 78 <223> OTHER INFORMATION: DISD22\_0011793  
 80 <220> FEATURE:  
 81 <223> OTHER INFORMATION: Located on chromosome 1  
 83 <220> FEATURE:  
 84 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 85 chromosomal short arm and 5'-terminus of this base  
 86 sequence : 100269  
 88 <220> FEATURE:  
 89 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 90 sequence listing upward to telomere on chrosomal short arm and  
 91 5'-terminus of this base sequence : 91592  
 93 <400> SEQUENCE: 2  
 94 aaccagtgc tagcagacgc cgtccctcag gatgcaggca cacgcacaca cacacacaca 60  
 96 cacatgcaca cgcacacaca tgaacacaca tggacacgcg aacacacaca tgcacacgta 120  
 98 cacacgtgt ctgacacgcg gatgctggc cagggctcac cactccaacg cggggtcctg 180  
 100 gcagccccagc gggtaccaga gctcaat 207  
 103 <210> SEQ ID NO: 3  
 104 <211> LENGTH: 271  
 105 <212> TYPE: DNA  
 106 <213> ORGANISM: Homo sapiens  
 108 <220> FEATURE:  
 109 <223> OTHER INFORMATION: DIS07\_10007615  
 111 <220> FEATURE:  
 112 <223> OTHER INFORMATION: Located on chromosome 1  
 114 <220> FEATURE:  
 115 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 116 chromosomal short arm and 5'-terminus of this base  
 117 sequence : 706251  
 119 <220> FEATURE:  
 120 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 121 sequence listing upward to telomere on chrosomal short arm and  
 122 5'-terminus of this base sequence : 605775  
 124 <400> SEQUENCE: 3  
 125 tgtgaacttc aaactctcag ggtttctga ggaataaaga gggttttgc aaaatggagt 60  
 127 cagggtcgcc ttctgtttt tcttctttc tttctttt ttttttttt ttgagaagga 120  
 129 gcctcgctc gtcccaaggt tggagtgcaa tggcaggatc ttgctcact gcaacctctg 180  
 131 cctcccggt tcaagtgatt ctctacctc gcctcctgag tagctggac tacaagcacg 240  
 133 tgccatgtgt agagatggca tctcaactgtg 271  
 136 <210> SEQ ID NO: 4  
 137 <211> LENGTH: 123  
 138 <212> TYPE: DNA  
 139 <213> ORGANISM: Homo sapiens  
 141 <220> FEATURE:  
 142 <223> OTHER INFORMATION: DIS07\_10000554

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/674,124

DATE: 10/08/2003

TIME: 13:16:54

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

144 <220> FEATURE:  
 145 <223> OTHER INFORMATION: Located on chromosome 1  
 147 <220> FEATURE:  
 148 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 149 chromosomal short arm and 5'-terminus of this base  
 150 sequence : 1020587  
 152 <220> FEATURE:  
 153 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 154 sequence listing upward to telomere on chrosomal short arm and  
 155 5'-terminus of this base sequence : 314065  
 157 <400> SEQUENCE: 4  
 158 acgcagattg gtctgtcccc agagggcgct tggagggcag cgaaaggatt cgggcctgga 60  
 160 taggggcttg acctagccct cctcctcctc tcctcctcc tcctcgaagt gggcttgctt 120  
 162 ctt 123  
 165 <210> SEQ ID NO: 5  
 166 <211> LENGTH: 410  
 167 <212> TYPE: DNA  
 168 <213> ORGANISM: Homo sapiens  
 170 <220> FEATURE:  
 171 <223> OTHER INFORMATION: chrl.fa.07frz.1780396  
 173 <220> FEATURE:  
 174 <223> OTHER INFORMATION: Located on chromosome 1  
 176 <220> FEATURE:  
 177 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 178 chromosomal short arm and 5'-terminus of this base  
 179 sequence : 1105774  
 181 <220> FEATURE:  
 182 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 183 sequence listing upward to telomere on chrosomal short arm and  
 184 5'-terminus of this base sequence : 85064  
 186 <400> SEQUENCE: 5  
 187 gctaacttgc atcttttagtc acatgcaaag agaaaaaaac cagacggact tctttttcat 60  
 189 agttaatagc agaaattatt atagcactct gctgtccaa catttgagtt tcaattcaga 120  
 191 gactcaaaac ctacgttgtt caatttttt taaaaaggcg tattcctggc tgggcattggt 180  
 193 gggctataat cccaacactt taggaggtca agtcgggagg actgcttcaa tccagcagtt 240  
 195 tgcgaccagc ctgggcaata tggcaaaacg ctgtgtacac acacacatac acacatacac 300  
 197 acacacacac acacaatttt tggtagcaat aaaaataaaat ttcctggtca ggccctttc 360  
 199 agtccacacaca tagaagtgtat aagaaaaatc tattgtcagg catttcaatt 410  
 202 <210> SEQ ID NO: 6  
 203 <211> LENGTH: 102  
 204 <212> TYPE: DNA  
 205 <213> ORGANISM: Homo sapiens  
 207 <220> FEATURE:  
 208 <223> OTHER INFORMATION: DISD22\_0011809  
 210 <220> FEATURE:  
 211 <223> OTHER INFORMATION: Located on chromosome 1  
 213 <220> FEATURE:  
 214 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 215 chromosomal short arm and 5'-terminus of this base

## RAW SEQUENCE LISTING

DATE: 10/08/2003

PATENT APPLICATION: US/10/674,124

TIME: 13:16:54

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

216 sequence : 1238096  
 218 <220> FEATURE:  
 219 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 220 sequence listing upward to telomere on chrosomal short arm and  
 221 5'-terminus of this base sequence : 131912  
 223 <400> SEQUENCE: 6  
 224 cagaggacgc agagctaaga aagtggac cttttttt tcagcactac acacacacac 60  
 226 acacacacga actgcagggg gctctggagc catggagttt ga 102  
 229 <210> SEQ ID NO: 7  
 230 <211> LENGTH: 162  
 231 <212> TYPE: DNA  
 232 <213> ORGANISM: Homo sapiens  
 234 <220> FEATURE:  
 235 <223> OTHER INFORMATION: D1S243  
 237 <220> FEATURE:  
 238 <223> OTHER INFORMATION: Located on chromosome 1  
 240 <220> FEATURE:  
 241 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 242 chromosomal short arm and 5'-terminus of this base  
 243 sequence : 1525955  
 245 <220> FEATURE:  
 246 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 247 sequence listing upward to telomere on chrosomal short arm and  
 248 5'-terminus of this base sequence : 287757  
 250 <400> SEQUENCE: 7  
 251 gctccagcgt catggacttt tccggcattt ggtcgaggcc tcagcgattc aggcggggcc 60  
 253 gttttggtaa caccctgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg 120  
 255 tccgtgcgcg cgccatgcg tgcaaggcatg tgacgcgttg tg 162  
 258 <210> SEQ ID NO: 8  
 259 <211> LENGTH: 283  
 260 <212> TYPE: DNA  
 261 <213> ORGANISM: Homo sapiens  
 263 <220> FEATURE:  
 264 <223> OTHER INFORMATION: DIS07\_10007619  
 266 <220> FEATURE:  
 267 <223> OTHER INFORMATION: Located on chromosome 1  
 269 <220> FEATURE:  
 270 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 271 chromosomal short arm and 5'-terminus of this base  
 272 sequence : 1667184  
 274 <220> FEATURE:  
 275 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 276 sequence listing upward to telomere on chrosomal short arm and  
 277 5'-terminus of this base sequence : 141067  
 279 <400> SEQUENCE: 8  
 280 ctgtcaccga gaaggacact gggctggcct ttcctttgcc tttttaata ttttattttta 60  
 282 ttttatattt tattttattt tattttattt tattttattt attttattttt attttatttt 120  
 284 attttattttt attttattttt aatcatagag atggggcctc cctttgtggc ccaggctggc 180  
 286 cttaactcc tgagttcaag caatccccc gcctcagcct cccaaagtgc tggatcact 240

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/674,124

DATE: 10/08/2003  
TIME: 13:16:54

Input Set : D:\seqlist.txt  
Output Set: N:\CRF4\10082003\J674124.raw

288 ggctggccc cgcccaagct cccctgcctt tcctgaggca tag 283  
 291 <210> SEQ ID NO: 9  
 292 <211> LENGTH: 260  
 293 <212> TYPE: DNA  
 294 <213> ORGANISM: Homo sapiens  
 296 <220> FEATURE:  
 297 <223> OTHER INFORMATION: DISD22\_0011823  
 299 <220> FEATURE:  
 300 <223> OTHER INFORMATION: Located on chromosome 1  
 302 <220> FEATURE:  
 303 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 304 chromosomal short arm and 5'-terminus of this base  
 305 sequence : 2173981  
 307 <220> FEATURE:  
 308 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 309 sequence listing upward to telomere on chrosomal short arm and  
 310 5'-terminus of this base sequence : 506514  
 312 <400> SEQUENCE: 9  
 313 tccatcagtc tagctggaaat atttttagta aaaaaaggct gtgtgtgtgt gtgtgtgtgt 60  
 315 gtgtgtgtgt gtgtgtgtgt gtctgtctgt ctgtctgtct gtctgcctag gtagatggat 120  
 317 ggagaaaatgg gcggatggat gaatgggtgg atggatggat agatggatag atgaatgaat 180  
 319 ggacagatgg atatgtgagt gtgtgtgtgt gtgtgtgtct gtctgtctgtct gtctgtctgt 240  
 321 gtagtcagat ggataaaatgc 260  
 324 <210> SEQ ID NO: 10  
 325 <211> LENGTH: 142  
 326 <212> TYPE: DNA  
 327 <213> ORGANISM: Homo sapiens  
 329 <220> FEATURE:  
 330 <223> OTHER INFORMATION: DISD22\_0011835  
 332 <220> FEATURE:  
 333 <223> OTHER INFORMATION: Located on chromosome 1  
 335 <220> FEATURE:  
 336 <223> OTHER INFORMATION: Distance between a terminus base of telomere on  
 337 chromosomal short arm and 5'-terminus of this base  
 338 sequence : 2407733  
 340 <220> FEATURE:  
 341 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
 342 sequence listing upward to telomere on chrosomal short arm and  
 343 5'-terminus of this base sequence : 233492  
 345 <400> SEQUENCE: 10  
 346 gaaatttaggt caagacgtat gcatgtgcgt gtttgtgtgt gtgtgtgtgt gtgtgtgtgt 60  
 348 gtgttggttt attgctcatg aaagcagatt tgaatttctt ttaagagtgt agccaattct 120  
 350 ctcattatcc aactcagttt cc 142  
 353 <210> SEQ ID NO: 11  
 354 <211> LENGTH: 245  
 355 <212> TYPE: DNA  
 356 <213> ORGANISM: Homo sapiens  
 358 <220> FEATURE:  
 359 <223> OTHER INFORMATION: DISO7\_10007628

10/6/4, 124  
page 6

<210> 27089

<211> 28

<212> DNA

<213> Artificial

See page 8 on error  
summary report

<400> 27089

aatagccatg agaagctatg tgggggag

28

<210> 27090

<211> 29

<212> DNA

<213> Artificial

<400> 27090

ctacctcctt gccaaacttg ctgtttgtg

The type of errors shown exist throughout  
the sequence listing. Please check subsequent  
sequences for similar errors.

<210> 863

<211> 201

<212> DNA

<213> Homo sapiens

<220>

<223> DISD22\_0000537

<220>

<223> Located on chromosome 1

<220>

<223> Distance between a terminus base of telomere on chromosomal short arm and 5'-terminus of this base sequence : 90759656

<220>

<223> Distance between 3'-terminus of neighbour sequence of sequence listing upward to telomere on chrosomal short arm and 5'-terminus of this base sequence : 295398

<400> 863

ttctccttca gaccctctga aaaaaaatgt taccttttg aggtggctc tctattttt 60

tctcccttagc ccctatgttt taaaaaaagct aag~~gt~~gtgtgt gtgtgtgtgt gtgtgtgtgt 120

gtgtgtgtgt gtgtgtgttt tgaagggagc aggcacaaaa gggaggggag tggaaagtaa 180

ttattatcat cccaacgtct t 201

NO explanation given for "n"

See item 9 on error summary sheet.

<210> 912  
 <211> 259  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <223> AL157410.5\_47389  
  
 <220>  
 <223> Located on chromosome 1  
  
 <220>  
 <223> Distance between a terminus base of telomere on  
 chromosomal short arm and 5'-terminus of this base  
 sequence : 96466263

<220>  
 <223> Distance between 3'-terminus of neighbour sequence of  
 sequence listing upward to telomere on chrosomal short arm and  
 5'-terminus of this base sequence : 97275

<400> 912	
gacactcagc ctcatcgagg atgcagagag aaaataactc gatggagaga agcaaggatt	60
aggggggtta aatgaccagg ttgggtgggg gaattaaatt atagacggtc ttaaaaaaca	120
ggcaggggag gttttctgt ttttgt <sup>n</sup> tc gttttgtttt gttttgtttt gttttgtttt	180
aaagacagga tcgcactctg ttgcccaggc tggagtaca <sup>g</sup> tggcaccaac atagctcact	240
gtaacttcaa actccagga	259

Loss of n and / or Xaa has been detected in the  
 Sequence Listing. Review the Sequence Listing  
 to ensure a corresponding explanation is present  
 in the <220> to <223> fields of each sequence  
 using n or Xaa

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/674,124

DATE: 10/08/2003  
TIME: 13:16:55

Input Set : D:\seqlist.txt  
Output Set: N:\CRF4\10082003\J674124.raw

ase Note:

of n and/or Xaa have been detected in the Sequence Listing. Please review the  
uence Listing to ensure that a corresponding explanation is presented in the <220>  
<223> fields of each sequence which presents at least one n or Xaa.

#:28; N Pos. 34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53  
#:28; N Pos. 54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73  
#:28; N Pos. 74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93  
#:28; N Pos. 94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109  
#:28; N Pos. 110,111,112,113,114,115,116,117,118,119,120,121,122,123,124  
#:28; N Pos. 125,126,127,128,129,130,131,132,133  
#:863; N Pos. 94  
#:912; N Pos. 147  
#:3742; N Pos. 71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89  
#:3742; N Pos. 90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106  
#:3742; N Pos. 107,108,109,110,111,112,113,114,115,116,117,118,119,120  
#:3742; N Pos. 121,122,123,124,125,126,127,128,129,130,131,132,133,134  
#:3742; N Pos. 135,136,137,138,139,140,141,142,143,144,145,146,147,148  
#:3742; N Pos. 149,150,151,152,153,154,155,156,157,158,159,160,161,162  
#:3742; N Pos. 163,164,165,166,167,168,169,170  
#:3745; N Pos. 143,144  
#:3746; N Pos. 143,144  
#:4010; N Pos. 207,211,212,214,216,243,245,247,249,254,256,258,263,265  
#:4010; N Pos. 267,269,271,275,278  
#:4931; N Pos. 181,231,233  
#:4934; N Pos. 6  
#:4935; N Pos. 198  
#:4936; N Pos. 91,108  
#:5073; N Pos. 298  
#:5452; N Pos. 312  
#:5742; N Pos. 331,339  
#:5895; N Pos. 157,158,159,160,161,162,163,164,165,166,167,168,169,170  
#:5895; N Pos. 171,172,173,174,175,176,177,178,179,180,181,182,183,184  
#:5895; N Pos. 185,186,187,188,189,190,191,192,193,194,195,196,197,198  
#:5895; N Pos. 199,200,201,202,203,204,205,206,207,208,209,210,211,212  
#:5895; N Pos. 213,214,215,216,217,218,219,220,221,222,223,224,225,226  
#:5895; N Pos. 227,228,229,230,231,232,233,234,235,236,237,238,239,240  
#:5895; N Pos. 241,242,243,244,245,246,247,248,249,250,251,252,253,254  
#:5895; N Pos. 255,256  
#:5994; N Pos. 67  
#:6080; N Pos. 393,449  
#:6525; N Pos. 262,263,264,265,266,267,268,269,270,271,272,273,274,275  
#:6525; N Pos. 276,277,278,279,280,281,282,283,284,285,286,287,288,289  
#:6525; N Pos. 290,291,292,293,294,295,296,297,298,299,300,301,302,303  
#:6525; N Pos. 304,305,306,307,308,309,310,311,312,313,314,315,316,317  
#:6525; N Pos. 318,319,320,321,322,323,324,325,326,327,328,329,330,331  
#:6525; N Pos. 332,333,334,335,336,337,338,339,340,341,342,343,344,345  
#:6525; N Pos. 346,347,348,349,350,351,352,353,354,355,356,357,358,359  
#:6525; N Pos. 360,361

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/08/2003  
PATENT APPLICATION: US/10/674,124 TIME: 13:16:55

Input Set : D:\seqlist.txt  
Output Set: N:\CRF4\10082003\J674124.raw

# : 7259; N Pos. 59  
# : 7624; N Pos. 97, 99  
# : 7989; N Pos. 71  
# : 8303; N Pos. 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67  
# : 8303; N Pos. 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86  
# : 8303; N Pos. 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103  
# : 8303; N Pos. 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117

alid <213> Response:

of "Artificial" only as "<213> Organism" response is incomplete, 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

# : 27089, 27090, 27091, 27092, 27093, 27094, 27095, 27096, 27097, 27098, 27099, 27100  
#: 27101, 27102, 27103, 27104, 27105, 27106, 27107, 27108, 27109, 27110

of <220> Feature(NEW RULES):

uence(s) are missing the <220> Feature and associated headings. of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" Unknown". Please explain source of genetic material in <220> to <223> tion (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) c.1.823 of new Rules)

#:27089, 27090, 27091, 27092, 27093, 27094, 27095, 27096, 27097, 27098, 27099, 27100  
#:27101, 27102, 27103, 27104, 27105, 27106, 27107, 27108, 27109, 27110

VARIABLE LOCATION SUMMARY  
 PATENT APPLICATION: US/10/674,124

DATE: 10/08/2003  
 TIME: 13:16:55

Input Set : D:\seqlist.txt  
 Output Set: N:\CRF4\10082003\J674124.raw

of n's or Xaa's(NEW RULES):

of n's and/or Xaa's have been detected in the Sequence Listing.  
 of <220> to <223> is MANDATORY if n's or Xaa's are present.  
 <220> to <223> section, please explain location of n or Xaa, and which  
 idue n or Xaa represents.

```
#:28; N Pos. 34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53
#:28; N Pos. 54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73
#:28; N Pos. 74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93
#:28; N Pos. 94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109
#:28; N Pos. 110,111,112,113,114,115,116,117,118,119,120,121,122,123,124
#:28; N Pos. 125,126,127,128,129,130,131,132,133
#:863; N Pos. 94
#:912; N Pos. 147
#:3742; N Pos. 71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89
#:3742; N Pos. 90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106
#:3742; N Pos. 107,108,109,110,111,112,113,114,115,116,117,118,119,120
#:3742; N Pos. 121,122,123,124,125,126,127,128,129,130,131,132,133,134
#:3742; N Pos. 135,136,137,138,139,140,141,142,143,144,145,146,147,148
#:3742; N Pos. 149,150,151,152,153,154,155,156,157,158,159,160,161,162
#:3742; N Pos. 163,164,165,166,167,168,169,170
#:3745; N Pos. 143,144
#:3746; N Pos. 143,144
#:4010; N Pos. 207,211,212,214,216,243,245,247,249,254,256,258,263,265
#:4010; N Pos. 267,269,271,275,278
#:4931; N Pos. 181,231,233
#:4934; N Pos. 6
#:4935; N Pos. 198
#:4936; N Pos. 91,108
#:5073; N Pos. 298
#:5452; N Pos. 312
#:5742; N Pos. 331,339
#:5895; N Pos. 157,158,159,160,161,162,163,164,165,166,167,168,169,170
#:5895; N Pos. 171,172,173,174,175,176,177,178,179,180,181,182,183,184
#:5895; N Pos. 185,186,187,188,189,190,191,192,193,194,195,196,197,198
#:5895; N Pos. 199,200,201,202,203,204,205,206,207,208,209,210,211,212
#:5895; N Pos. 213,214,215,216,217,218,219,220,221,222,223,224,225,226
#:5895; N Pos. 227,228,229,230,231,232,233,234,235,236,237,238,239,240
#:5895; N Pos. 241,242,243,244,245,246,247,248,249,250,251,252,253,254
#:5895; N Pos. 255,256
#:5994; N Pos. 67
#:6080; N Pos. 393,449
#:6525; N Pos. 262,263,264,265,266,267,268,269,270,271,272,273,274,275
#:6525; N Pos. 276,277,278,279,280,281,282,283,284,285,286,287,288,289
#:6525; N Pos. 290,291,292,293,294,295,296,297,298,299,300,301,302,303
#:6525; N Pos. 304,305,306,307,308,309,310,311,312,313,314,315,316,317
#:6525; N Pos. 318,319,320,321,322,323,324,325,326,327,328,329,330,331
#:6525; N Pos. 332,333,334,335,336,337,338,339,340,341,342,343,344,345
#:6525; N Pos. 346,347,348,349,350,351,352,353,354,355,356,357,358,359
```

VARIABLE LOCATION SUMMARY  
PATENT APPLICATION: US/10/674,124

DATE: 10/08/2003  
TIME: 13:16:55

Input Set : D:\seqlist.txt  
Output Set: N:\CRF4\10082003\J674124.raw

#:6525; N Pos. 360,361  
#:7259; N Pos. 59  
#:7624; N Pos. 97,99  
#:7989; N Pos. 71  
#:8303; N Pos. 49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67  
#:8303; N Pos. 68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86  
#:8303; N Pos. 87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103  
#:8303; N Pos. 104,105,106,107,108,109,110,111,112,113,114,115,116,117

## VERIFICATION SUMMARY

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Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

3 M:270 C: Current Application Number differs, Replaced Current Application Number  
 37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
 38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0  
 41 Repeated in SeqNo=28  
 8637 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:863  
 8637 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:863  
 8637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:863 after pos.:60  
 0264 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:912  
 0264 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:912  
 0264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:912 after pos.:120  
 26228 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3742  
 26232 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3742  
 26235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3742 after pos.:60  
 41 Repeated in SeqNo=3742  
 26346 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3745  
 26346 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3745  
 26346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3745 after pos.:120  
 26383 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3746  
 26383 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3746  
 26383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3746 after pos.:120  
 35639 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4010  
 35639 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4010  
 35639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4010 after pos.:180  
 41 Repeated in SeqNo=4010  
 67364 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4931  
 67364 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4931  
 67364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4931 after pos.:180  
 67463 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4934  
 67463 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4934  
 67463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4934 after pos.:0  
 67504 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4935  
 67504 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4935  
 67504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4935 after pos.:180  
 67531 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4936  
 67531 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4936  
 67531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4936 after pos.:60  
 72172 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5073  
 72172 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5073  
 72172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5073 after pos.:240  
 85187 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5452  
 85187 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5452  
 85187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5452 after pos.:300  
 95157 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5742  
 95157 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5742  
 95157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5742 after pos.:300  
 00438 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5895  
 00438 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5895  
 00438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5895 after pos.:120

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41 Repeated in SeqNo=5895  
03877 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5994  
03877 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5994  
03877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5994 after pos.:60  
06835 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6080  
06835 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6080  
06835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6080 after pos.:360  
41 Repeated in SeqNo=6080  
21820 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6525  
21820 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6525  
21820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6525 after pos.:240  
41 Repeated in SeqNo=6525  
46228 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7259  
46228 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7259  
46228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7259 after pos.:0  
58531 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7624  
58531 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7624  
58531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7624 after pos.:60  
70586 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7989  
70586 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7989  
70586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7989 after pos.:60  
81124 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:8303  
81124 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8303  
81124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8303 after pos.:0  
41 Repeated in SeqNo=8303  
96787 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:8774  
96787 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8774  
96787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8774 after pos.:240  
07698 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9093  
07698 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9093  
07698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9093 after pos.:180  
09191 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9138  
09191 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9138  
09191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9138 after pos.:240  
52518 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13393  
52518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13393 after pos.:360  
53798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13431 after pos.:0  
65508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13779 after pos.:120  
69639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13900 after pos.:240  
71026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13941 after pos.:0  
71057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13942 after pos.:0  
41 Repeated in SeqNo=13942  
74427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14044 after pos.:0  
78017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14148 after pos.:0  
79327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14188 after pos.:0  
80750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14231 after pos.:60  
85639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14376 after pos.:0  
41 Repeated in SeqNo=14376  
89894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14501 after pos.:60

**VERIFICATION SUMMARY**

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92778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14587 after pos.:60  
00166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14805 after pos.:0  
00308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14809 after pos.:60  
00817 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14824 after pos.:60